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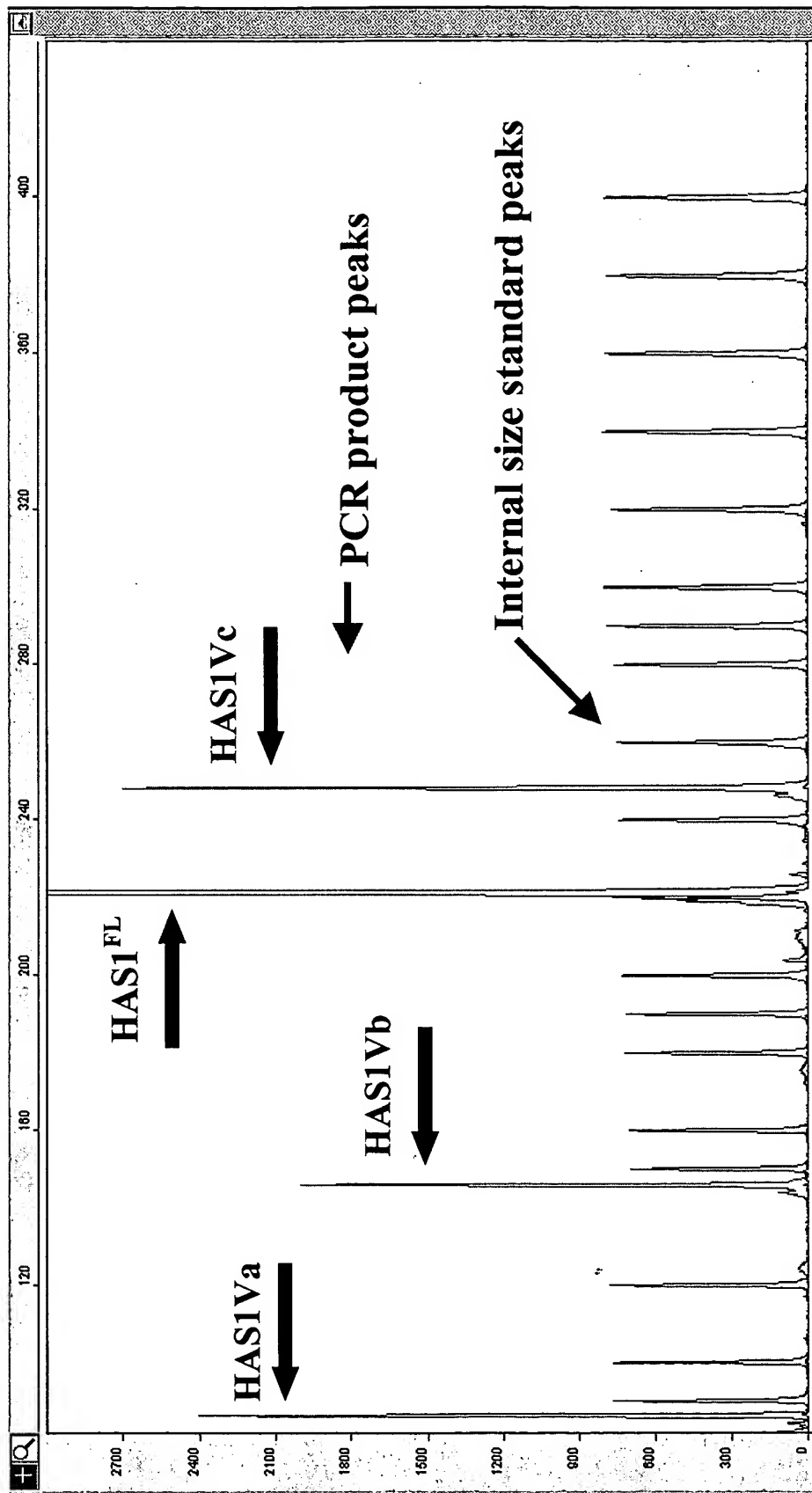
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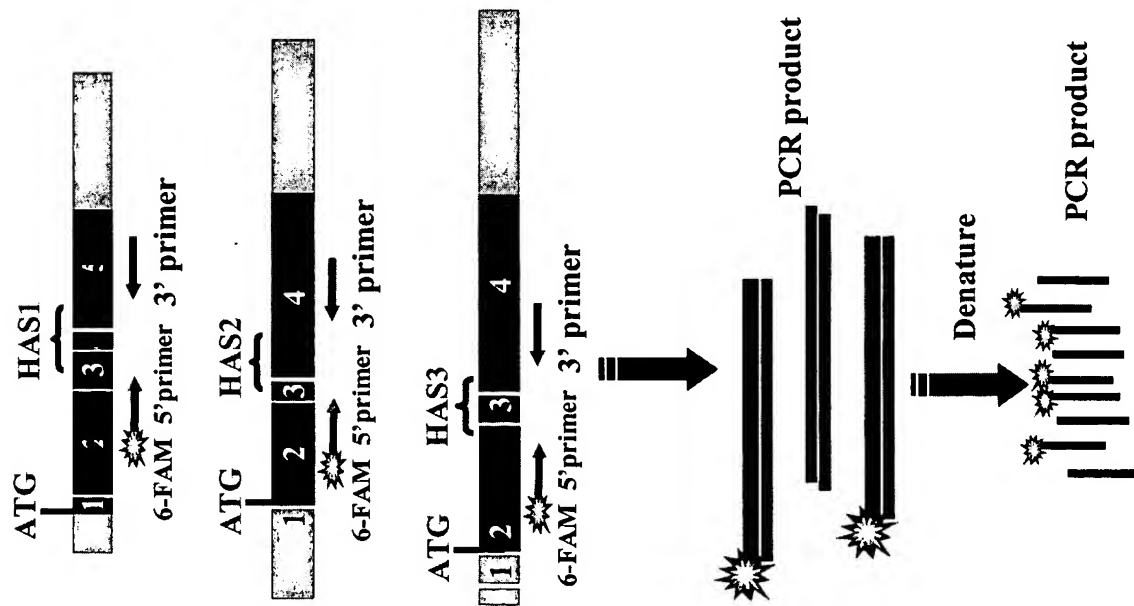
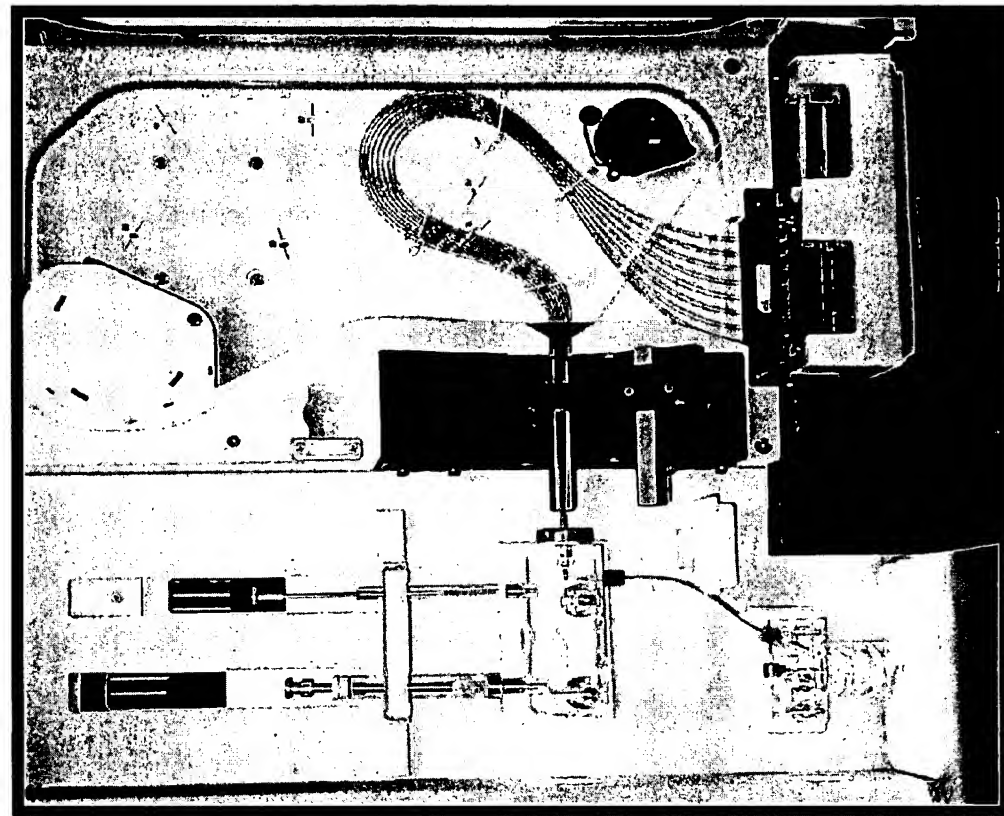
1/18

FIG 1



RFU- Relative Fluorescent Units

FIG 2



3100 Genetic Analyzer



FIG 3A

The x-axes represent molecular size (bp) of PCR product and the y-axes Relative Fluorescent units (RFU). —, — internal size standard peaks; — PCR product peaks.

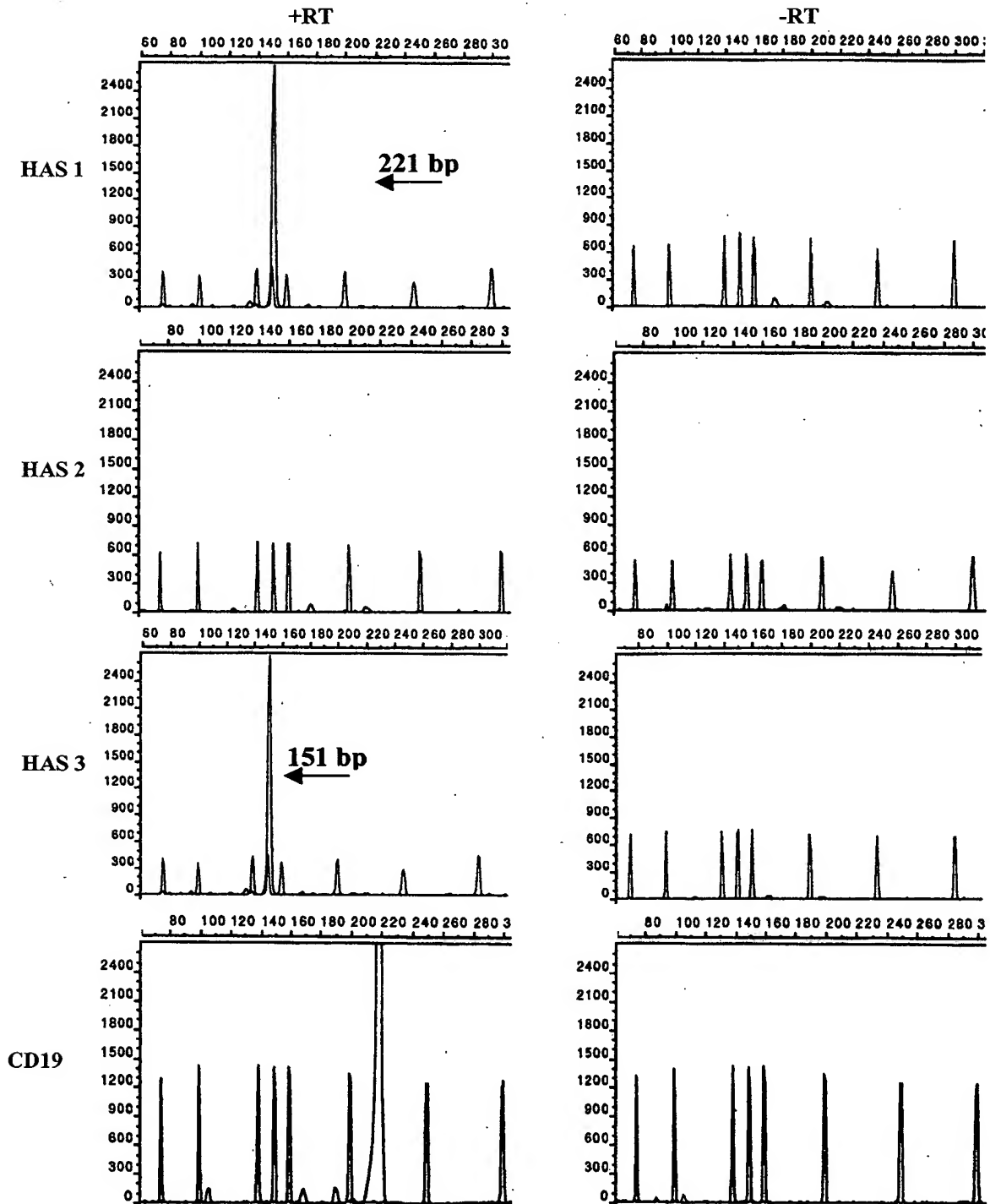


FIG 3B

The x-axes represent molecular size (bp) of PCR product and the y-axes Relative Fluorescent units (RFU). — internal size standard peaks; — PCR product peaks.

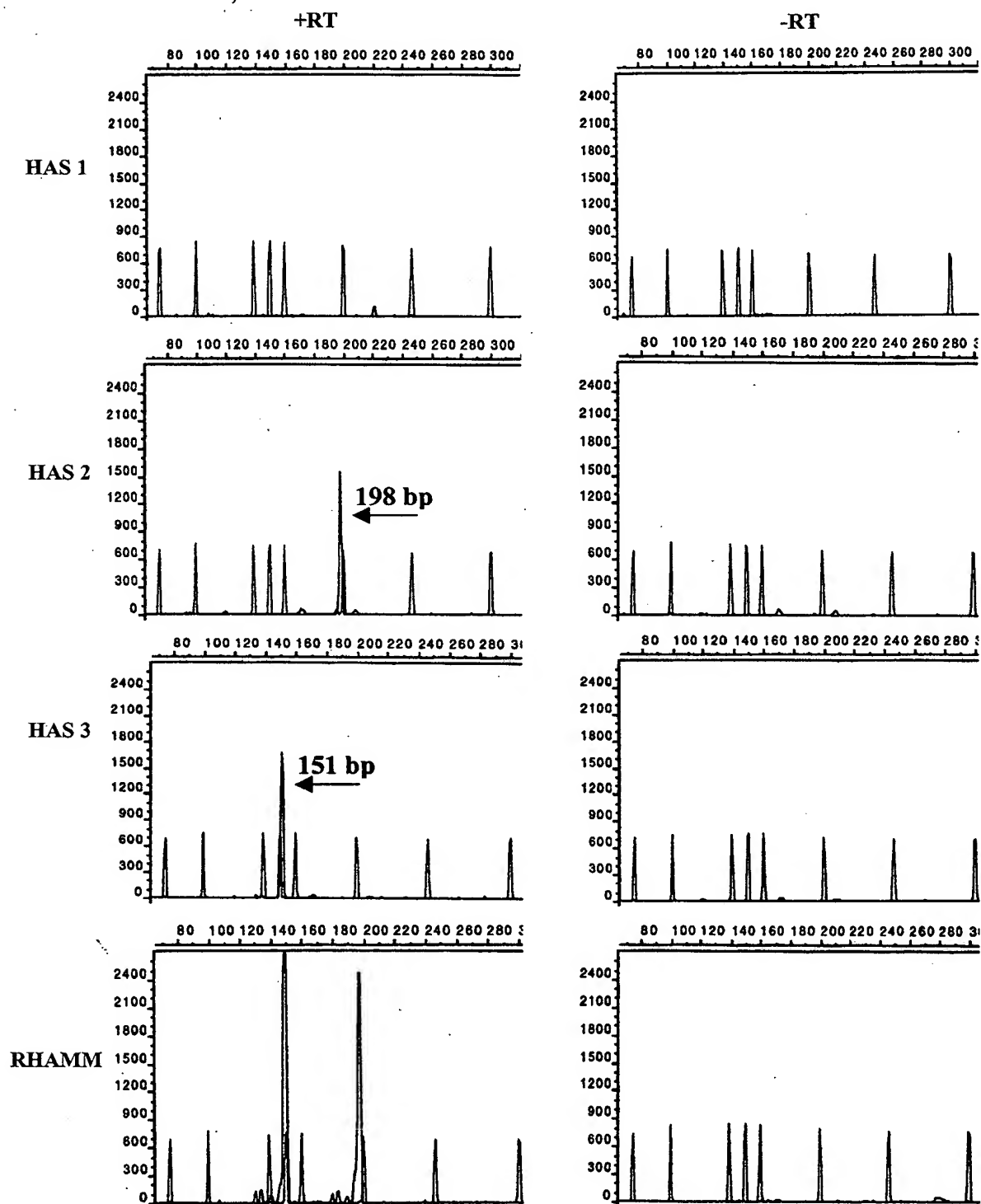


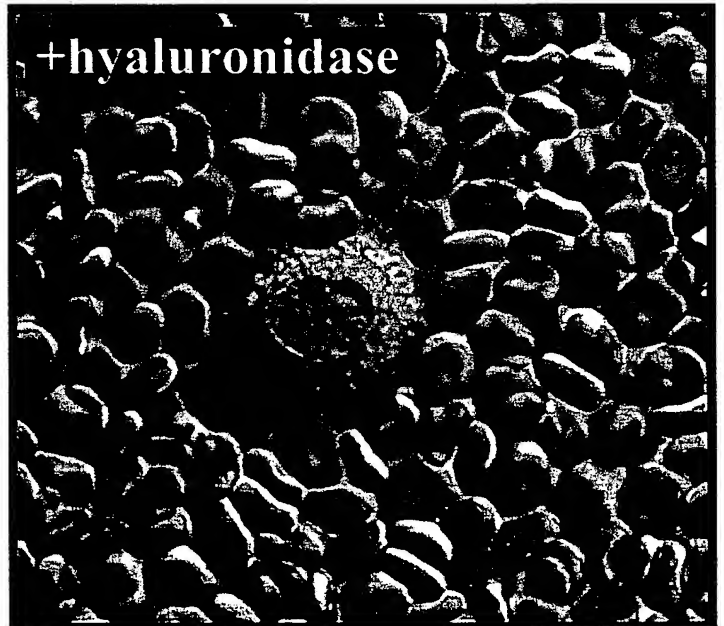
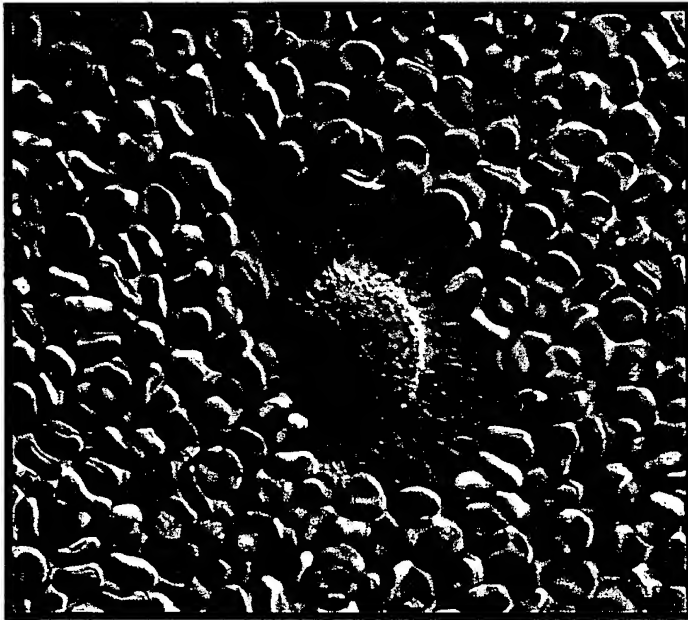
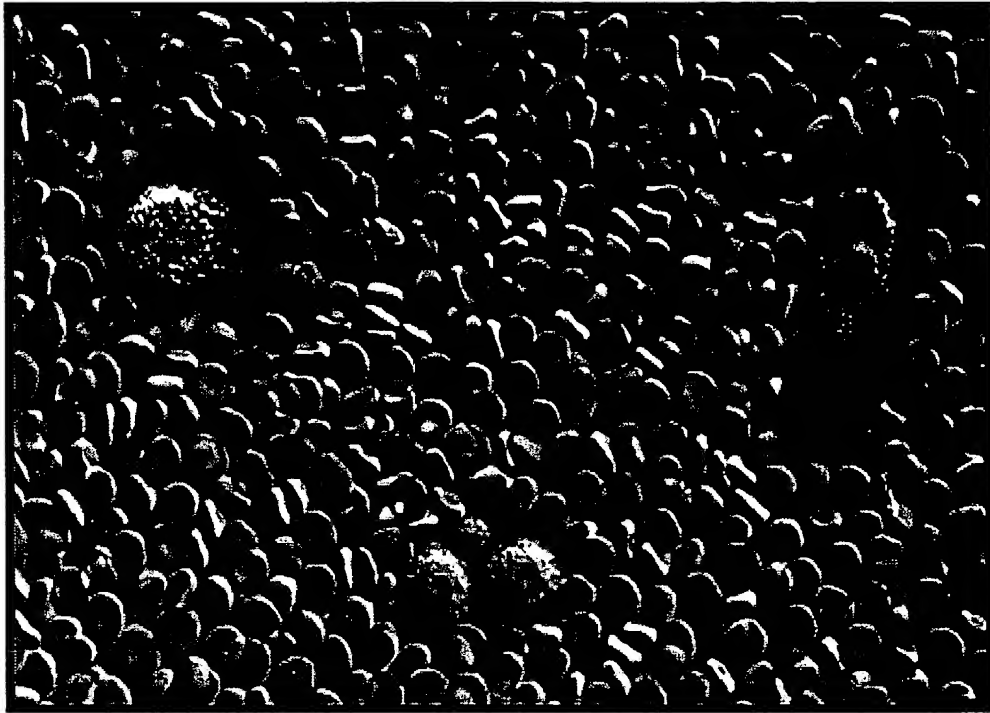
FIG 4A**MM B cells 48h after culturing**

FIG 4B

Particle Exclusion Assay in combination with HA staining

Sorted MM B cells \rightarrow Fixation with 2% PFA \rightarrow Indirect HA staining \rightarrow PEA

MM B 48h after culturing

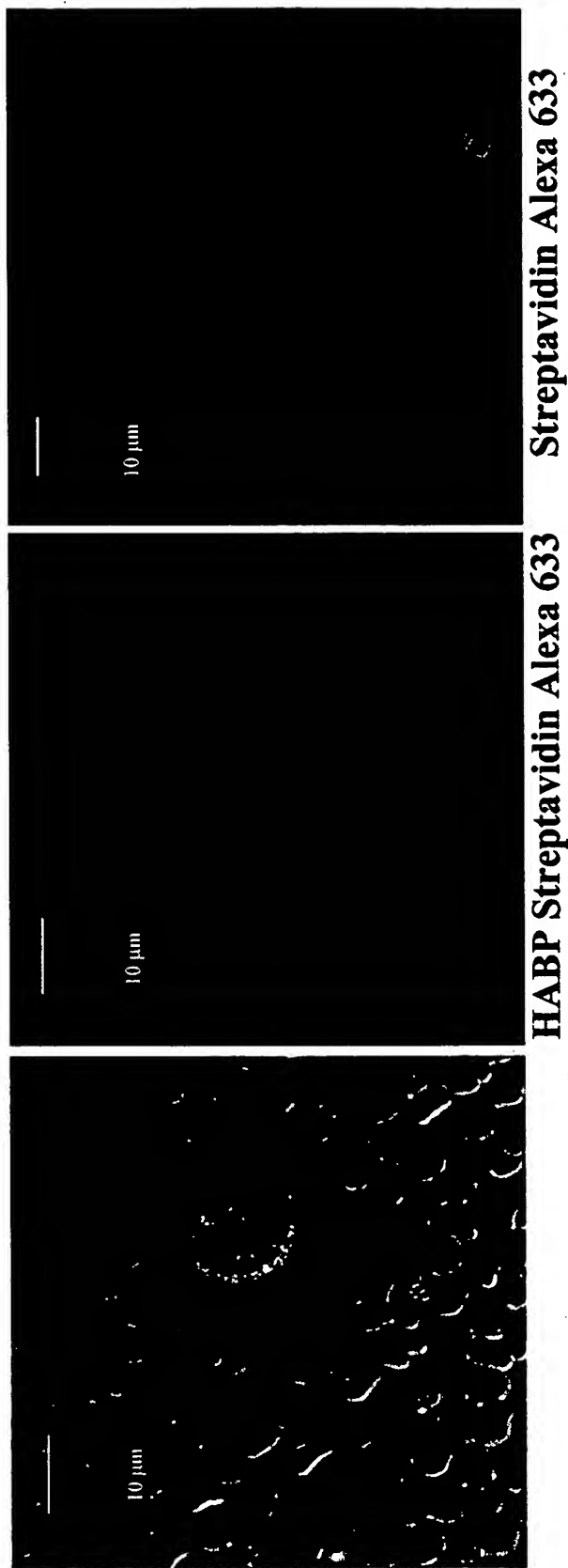
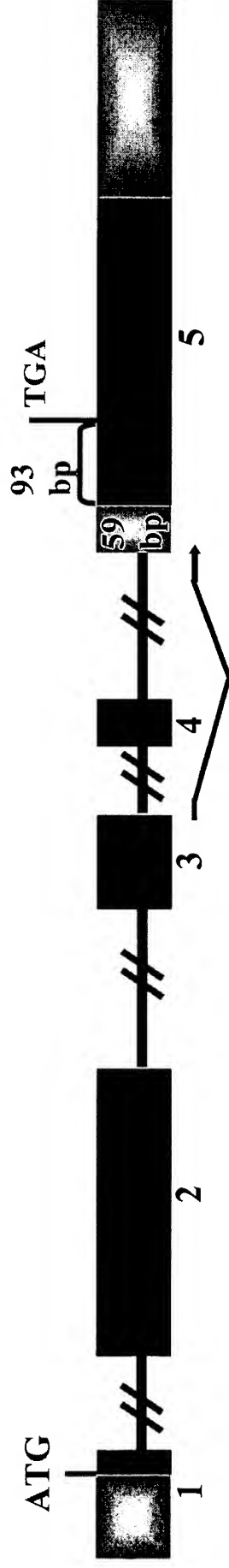


FIG 5B

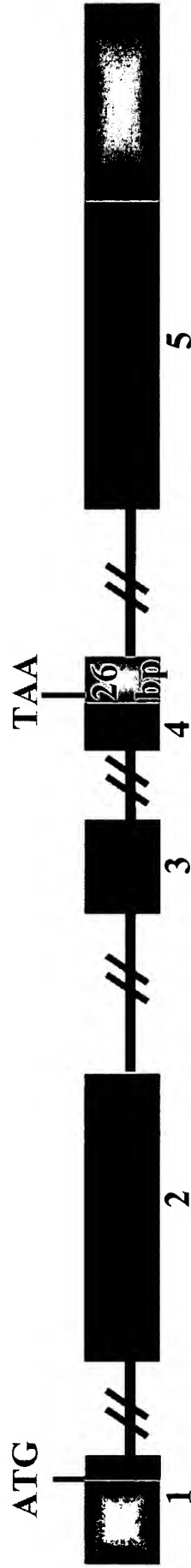
HAS 1Vb



HAS 1Vb - 361 aa - 39.52 KD

FIG 5C

HAS 1Vc



HAS 1Vc - 354/381 aa - ~36 KD

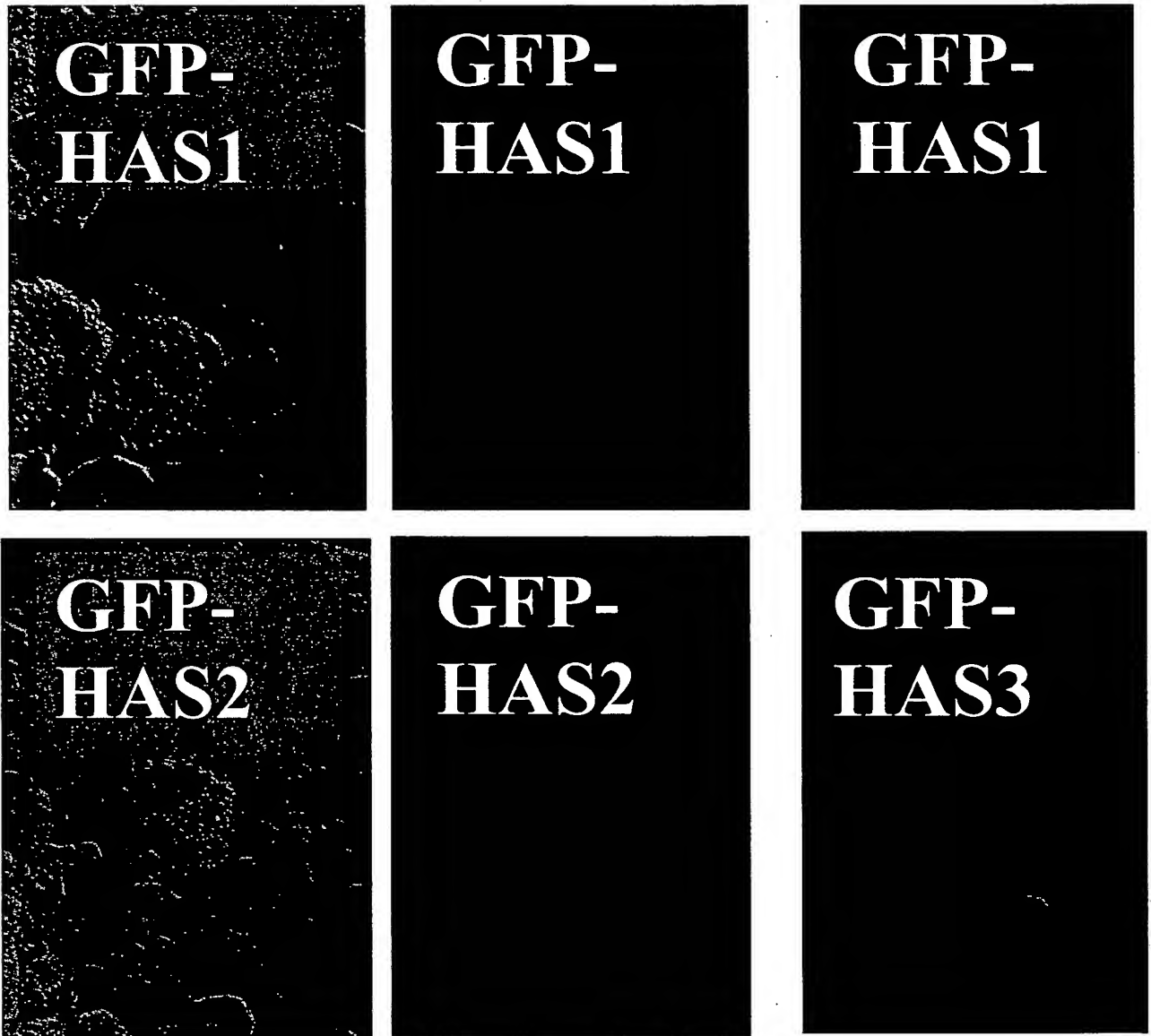
FIG 6

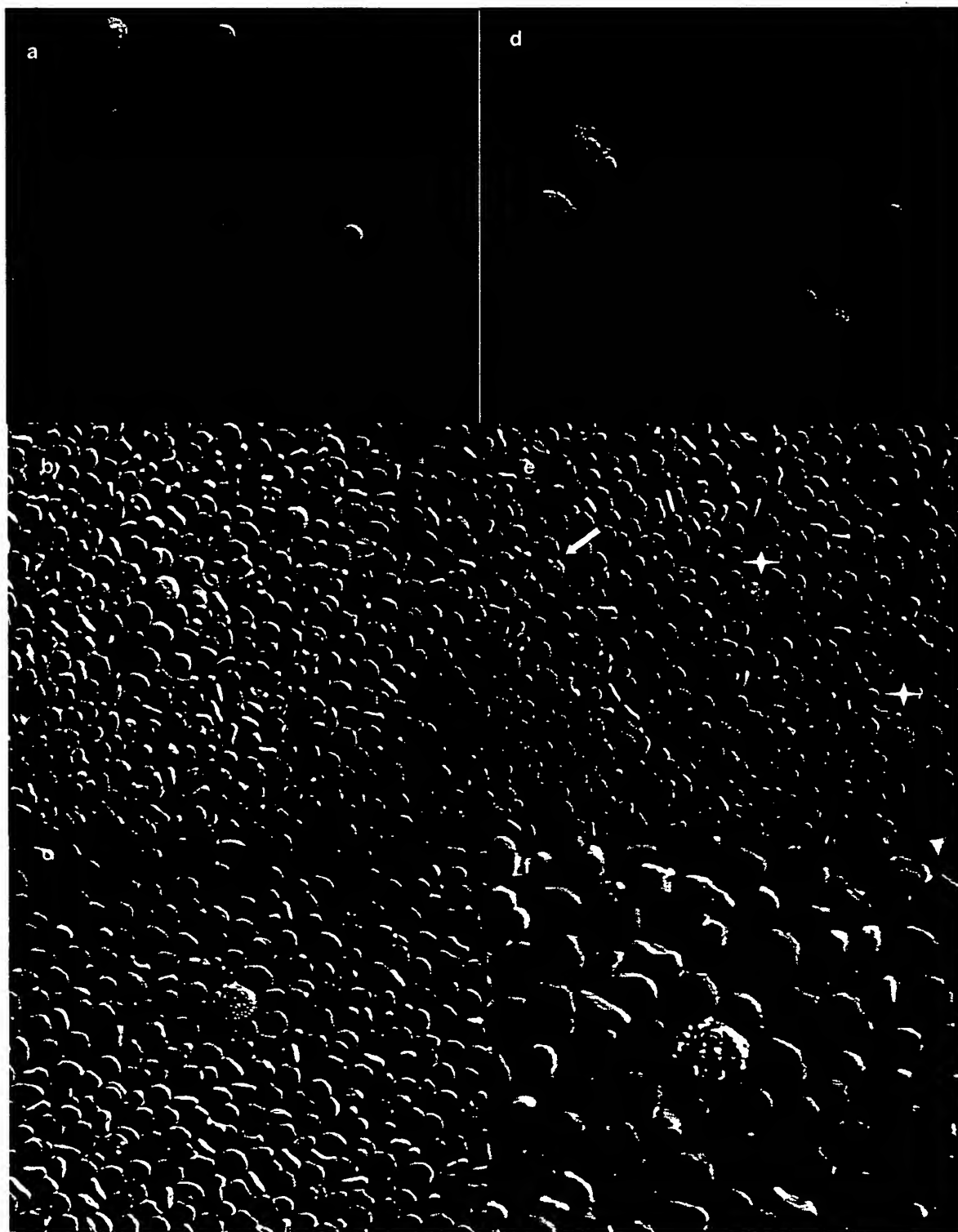
FIG 7

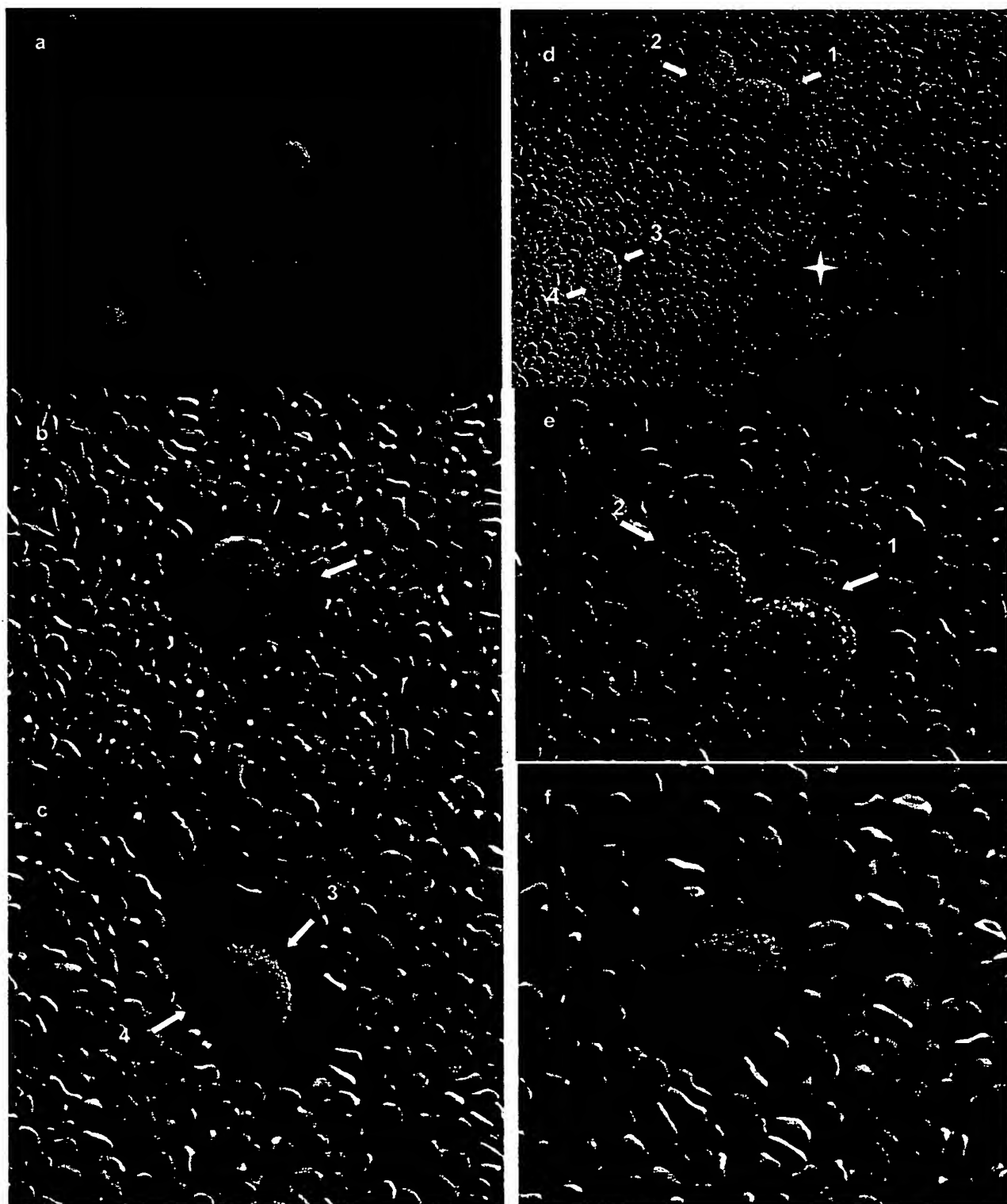
FIG 8

FIG 9.

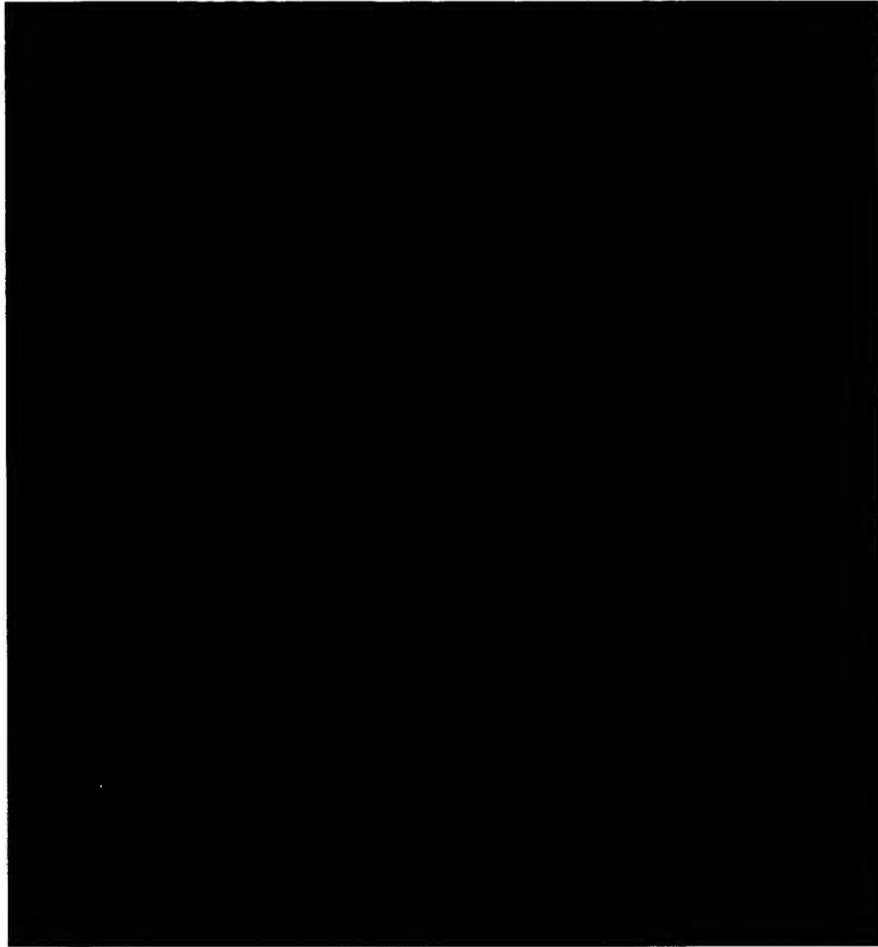
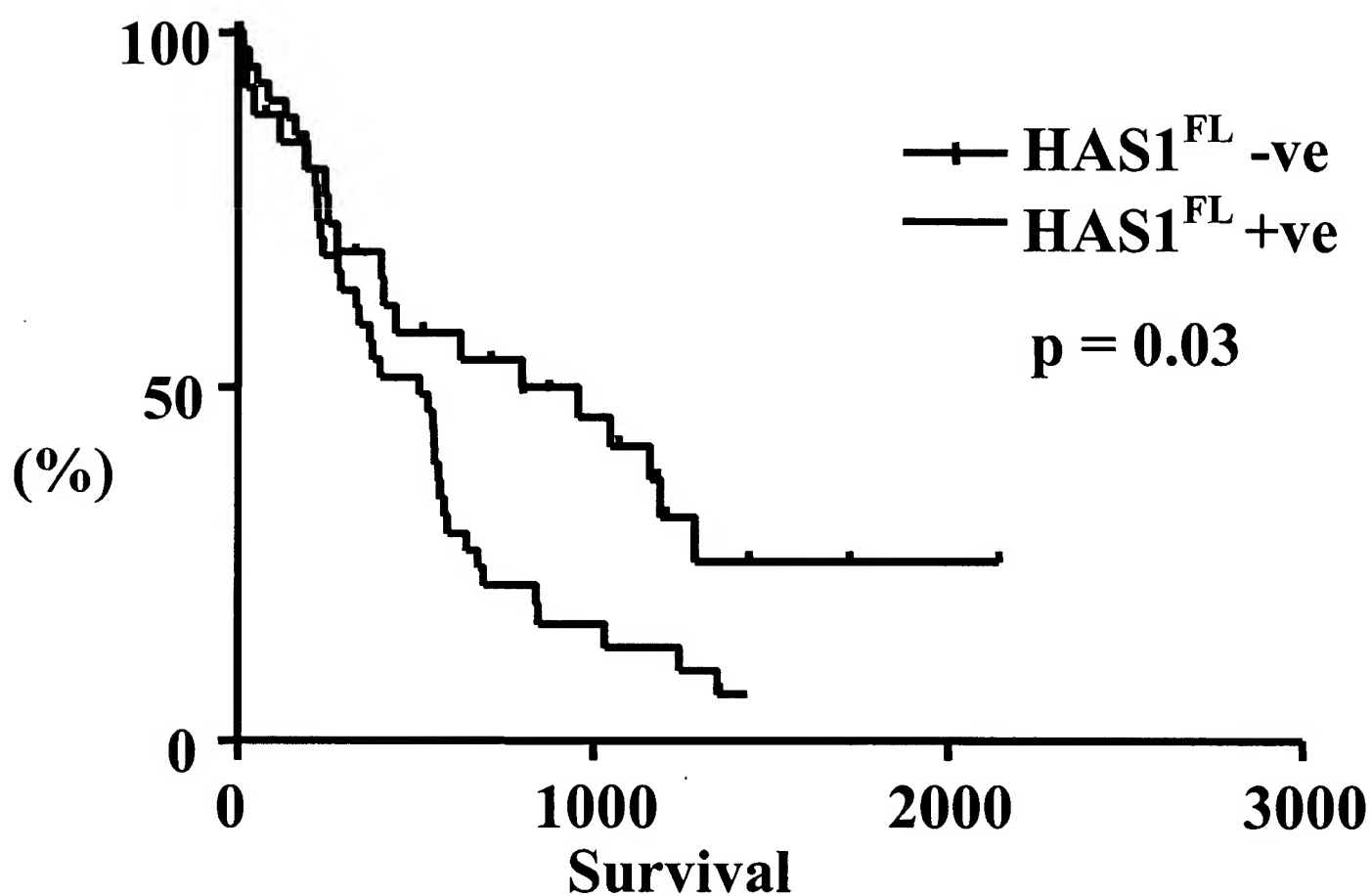
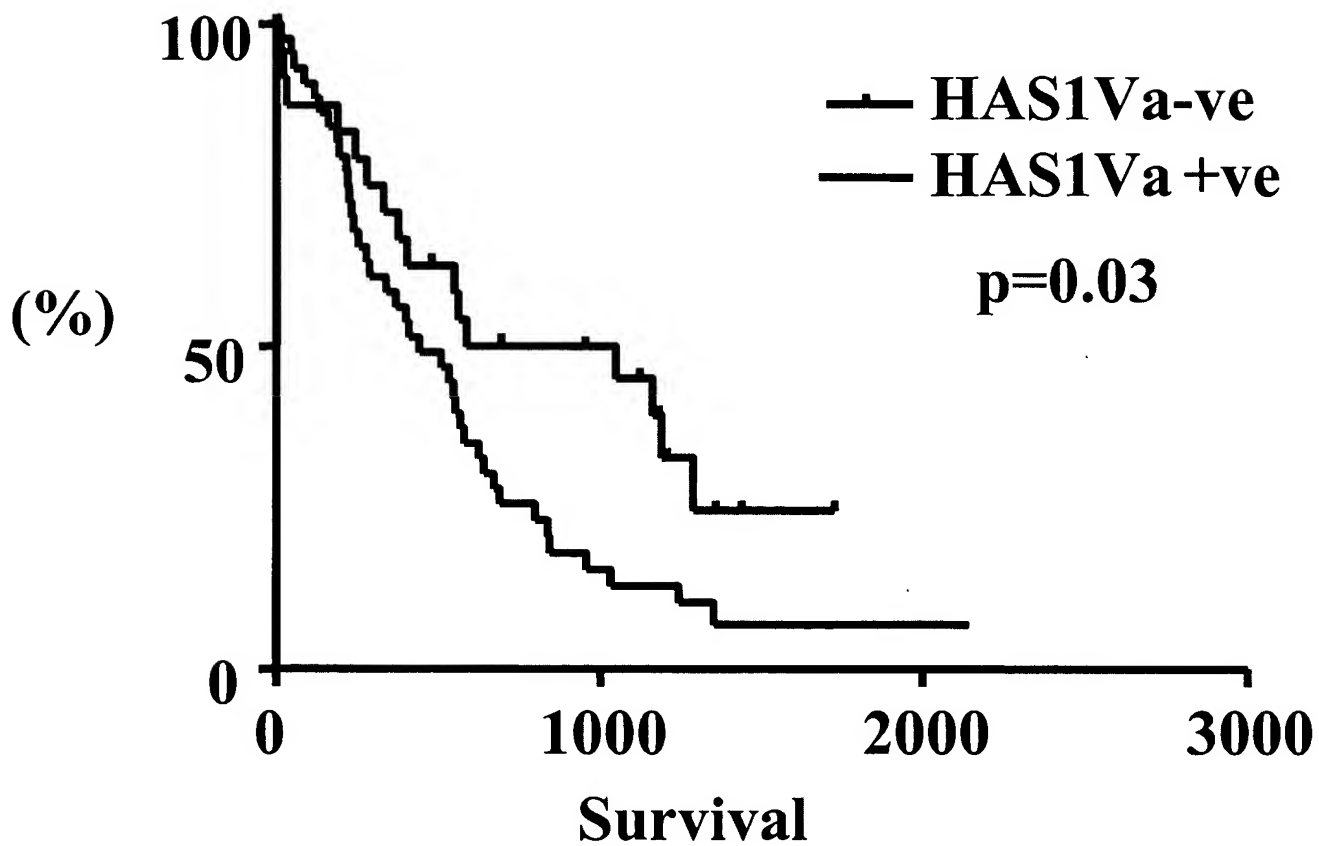


FIG 10

Overall Survival- HAS1^{FL}

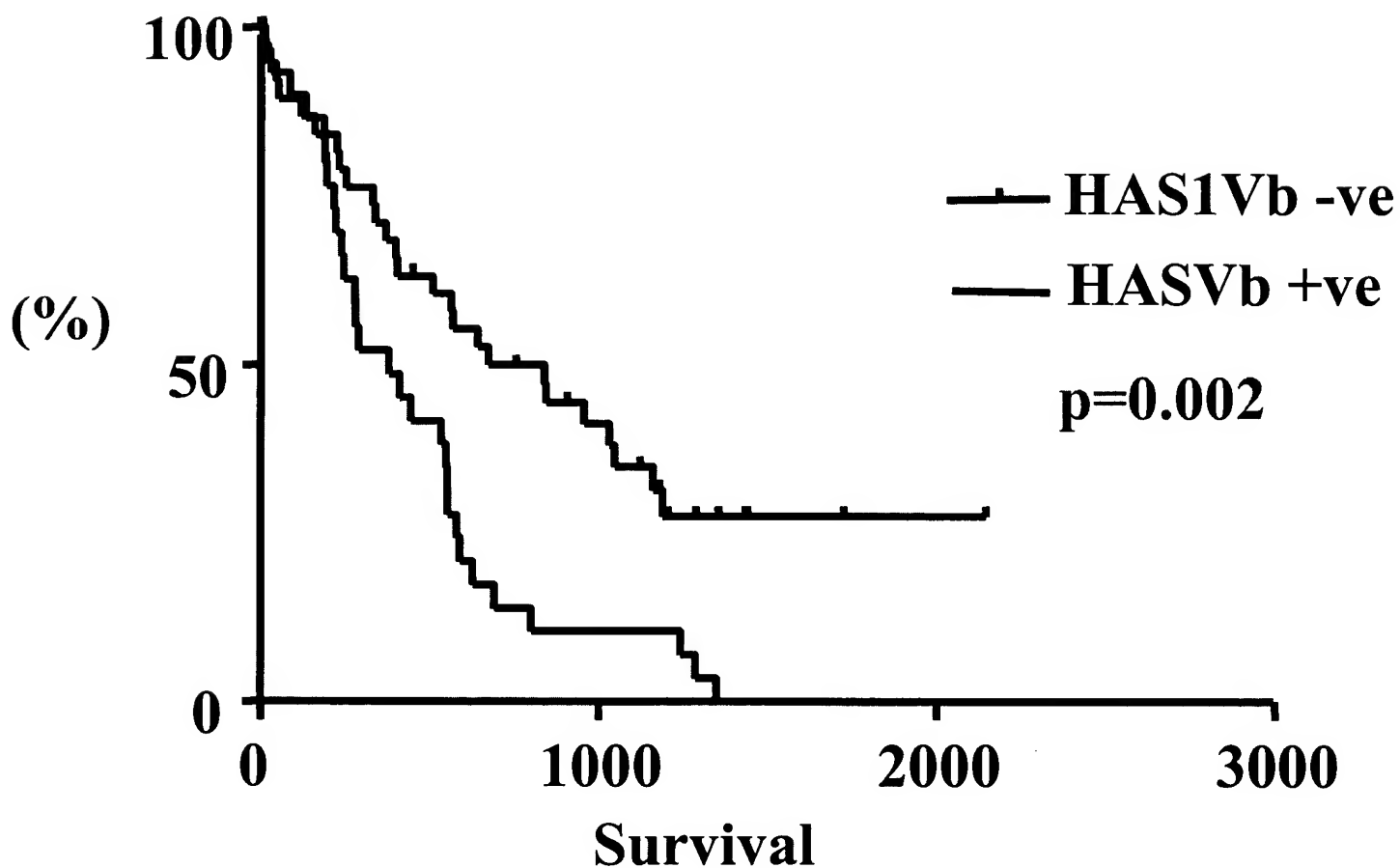


Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.03$, using the log rank test.

FIG 11**Overall Survival- HAS1Va**

Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.03$, using the log rank test.

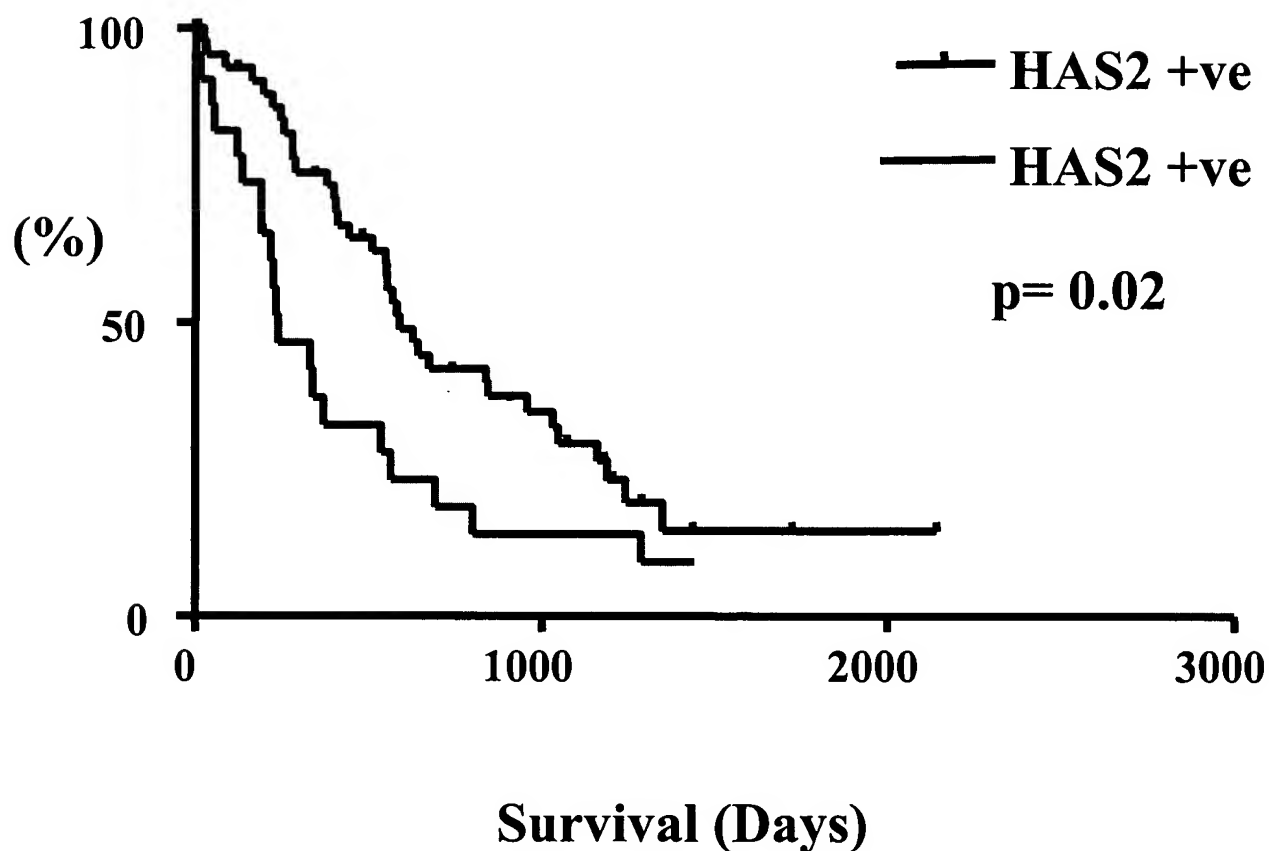
FIG 12

Overall Survival- HAS1Vb

Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.002$, using the log rank test.

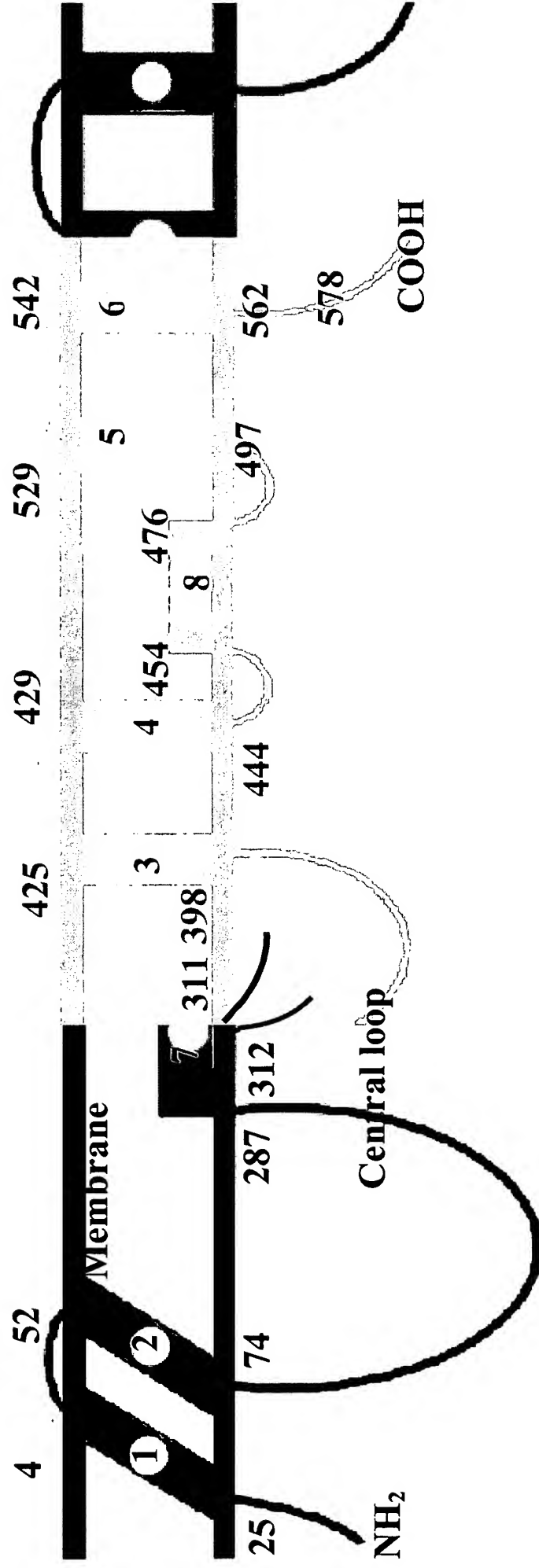
FIG 13

Overall Survival - HAS2



Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.02$, using the log rank test.

FIG 14



204-321aa - Glycosyl transferase 231-382aa - Chitin

Weigel, 1997; Heldermon et al., 2001

FIG 15

Secondary mRNA structure predicted

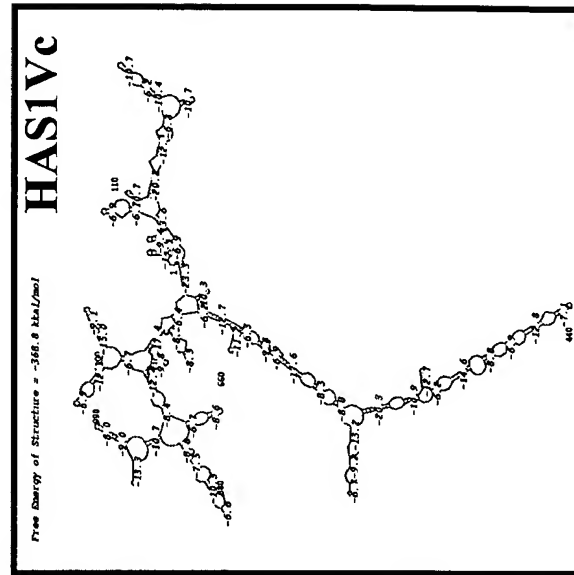
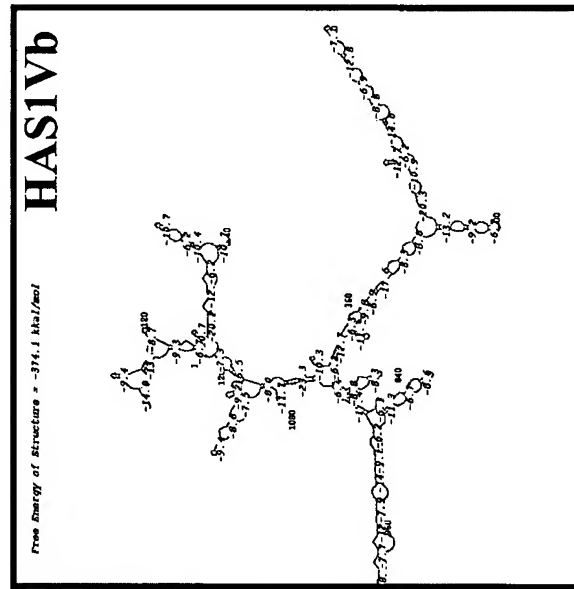
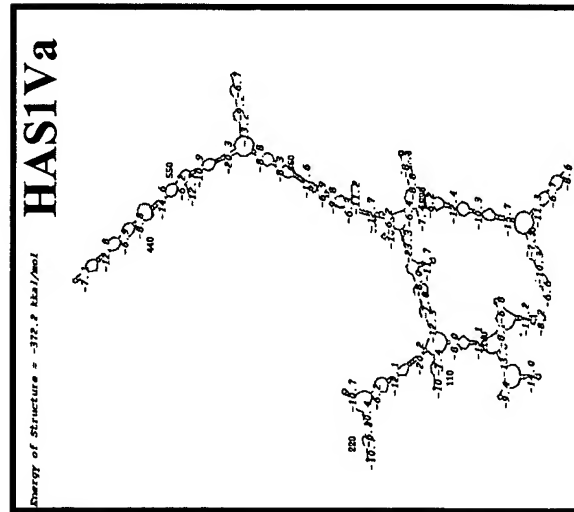
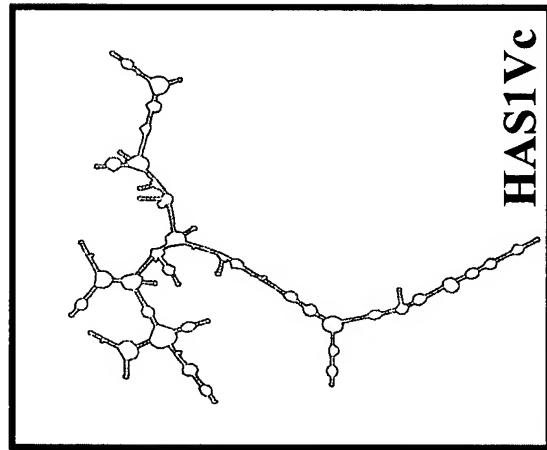
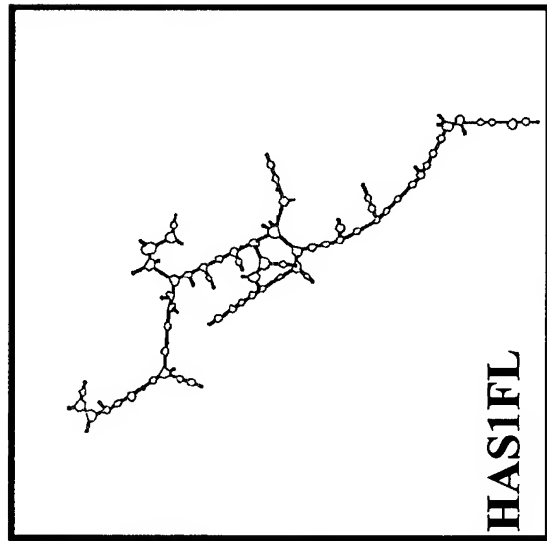


FIG 16

RT-PCR product analysis on microfluidic chip.

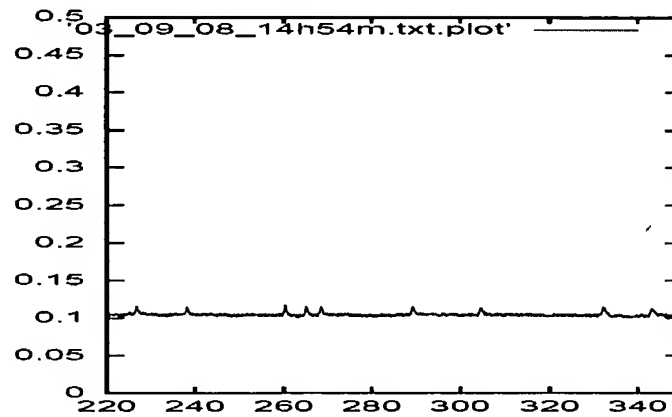
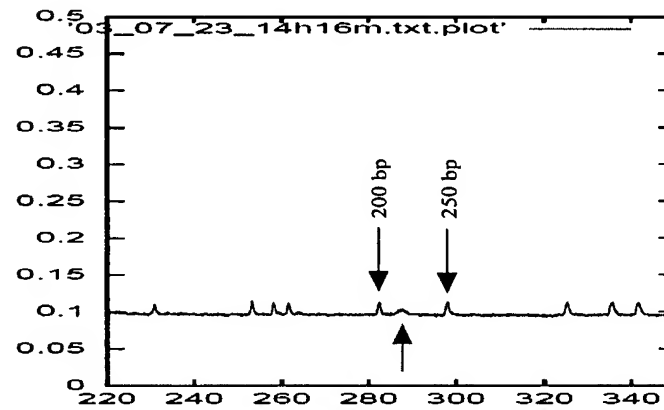
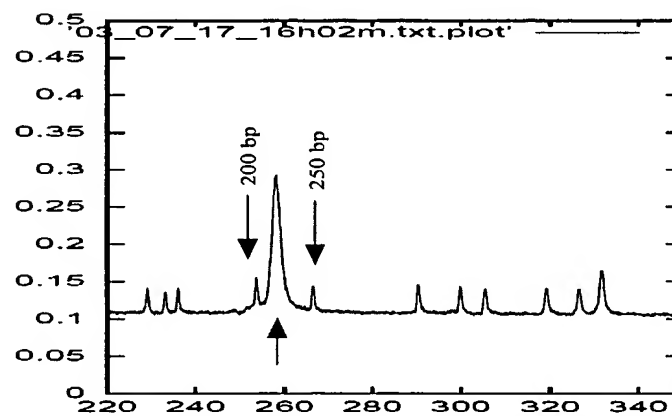
**Negative
Control****15 cycles****20 cycles**

FIG 17

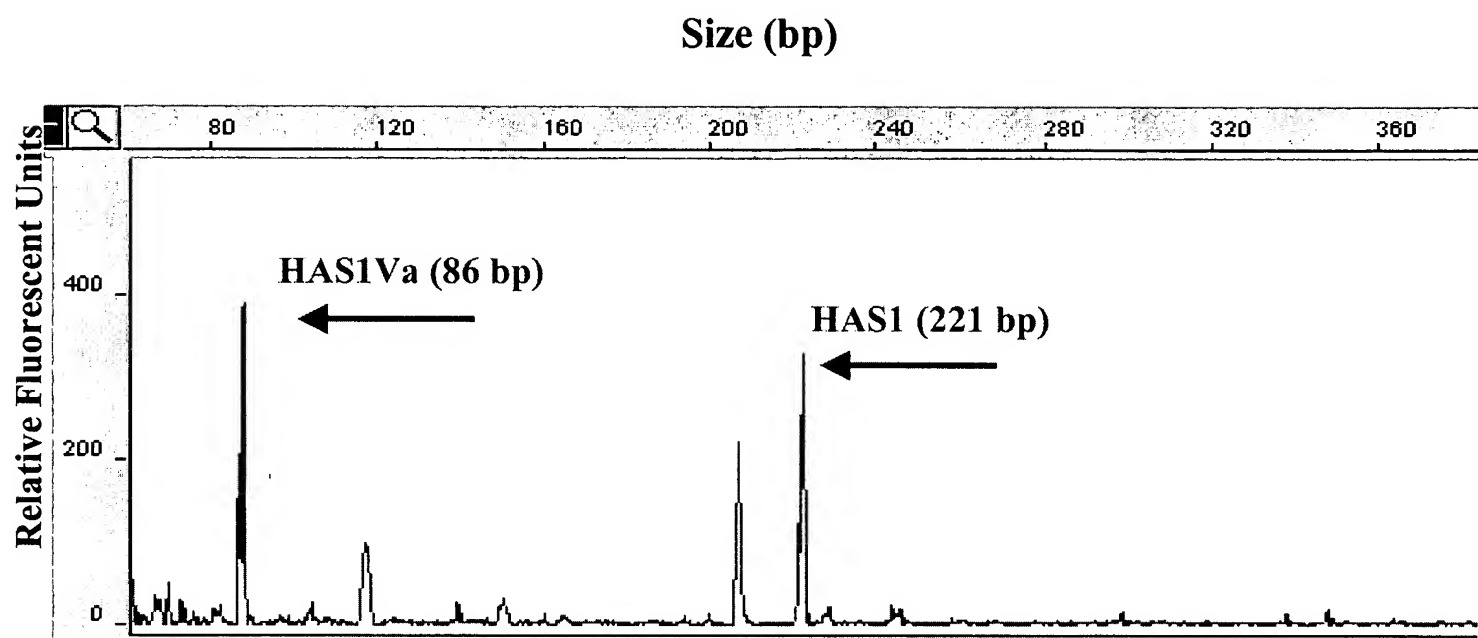


FIG 18

splice sites on intron 4 (fragment)

| | |
|------|--|
| 1 | taagctgag gggaccagggt ggtcggat gtgtggaggc caatgaatat cctagcgtgt gtgcatgctg agagtctctc aaatccaaag |
| 91 | taactcacca gacaatgggc tctatcaagt gagacttttag agggagagag aggataccat aatggggcaga gggggccattt gcattgagcc |
| 181 | aatggactct accaagttag atattaggga agaggggaag atactataag ggacaaggct ggcatttgca ttgaaccatg gaatgcggtg |
| 271 | aactctacca agagaggcaa gagggtgtagaatttcca cctagaatttg agataggag agtctggttct gtcatgggaga ccaaggtagc |
| 361 | acagtgggga gtgaagttag aagggcaaga gacaaatgga tagagtggga tctaactagt gagagagcca cggagagaaaga aacaagttag |
| 451 | agaagaggag cactgaact ctaaaagt cttcaagaga agacaagtaa ttccatgaga ctcaaggag gatgatctag accaagtga |
| 541 | gttcagggga gagtgtttc tgcaaaagcca ggtccactga aatacccaga ggaacttgg gataatccag gggaaatccat gcattaaatc |
| 631 | actcaacaaa tattcactag gtgcctagaa tgtttaagct gcggggatag agcaataggc agacaggaca ccaattgatt acatcagtctg |
| 721 | gggagacaca caagaaaataa ataagttagaa catacagtat gtccatgata tgtgttatgg agataaaataa tgccgggcaa ggttggtgga |
| 811 | taggaagtct tggggttggg ggtgaagtgt taagtggagt gcctgagaa ggatggggct caaggctgag aatagtgtgg ctgggagcact |
| 901 | gaactggggg agtattagga gagcaggatg gaggttaag gagtgttcca ctcatgaaag gcttataggt ctaaggactc tgactaaagt |
| 991 | gagggagcca tgggagggtt ttaagcagag aagtgcacg ttgtaatggg atccctctgg cagccgtttt gggtacagac tacaaaaaggc |
| 1081 | aaggtcggaa gcagggaggc cactgaggat gccaaagttag acagggggaag gagtctggac actgtcaagt aatgcccagg atctctctct |
| 1171 | tgtgtgggct tggctggaaa ccatgcaggg attgattaat gatgtctgcc acaaaaacagg aaggaggcct gatggttccc ttgagaagtt |
| 1261 | ctaatacata gactaccctg ggtagcaacc acaccatct tgcctctccc tatagggcct gccagtaata aagcatgg tagtattagt |
| 1351 | aatatgttag tgatagtatt agtaataag tcagttaacca acatgatatt agtaacagca atagttaatgg taacagcaat agtcatagta |
| 1441 | aaaacggtag tagctaact ttattgagca aatactatct actgggtccta agcacttggc gttaatttc attcaatcct tacatatatcc |
| 1531 | ttgtcttatg agagcctttt tttttttctt agtatagagtc ttgctgtgtt gctcaggtc ccaaatagct aggttgaggt gcaggggac gatcatggct |
| 1621 | cactgcagcc tcaaaactct gagctcaagt gatccccca tctcagcctc ccaaatagct gggactacag gccaccacgc ccggctaatt |
| 1711 | ttttttttt tttttttttt ttagagatgg ggtctcacta tgttgcttag aactctttag ctcaagttag cccctacct |
| 1801 | cagcctccta aagtgtctggg attacaggca tgaagcattg catcccaccc atttgtgtctt atttatttat ttattttatt atttagtga |
| 1891 | gatgggggtct tgctatgttg cccaggctgg tcttgaactc cttatccctc agcctcccaa agtgcctggga ttacaggagt gagccaccgc |
| 1981 | gtccaggcct aggaaccatt atccacccta ttctacacat gagaacactg aggcctagag aggttaagaa actcgcccc agtggccgtc |
| 2071 | cacagtggtc atttctgctt ccg |

■ donor splice sites (7) score (0.96-0.98) ■ acceptor splice sites (5) score (0.98-1)